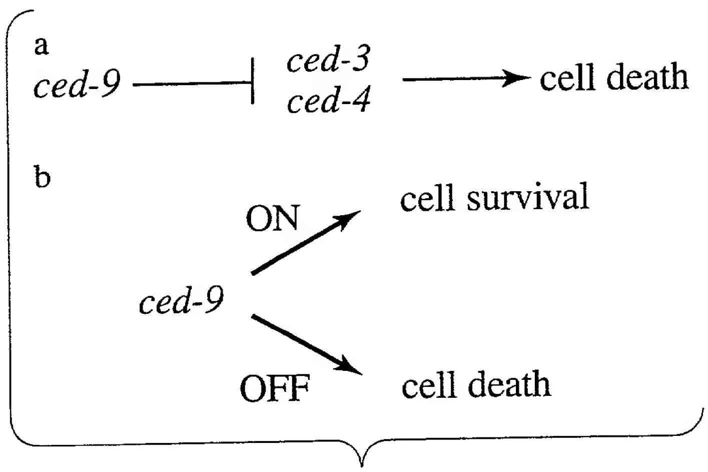
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cell death
b
ON
cell survival
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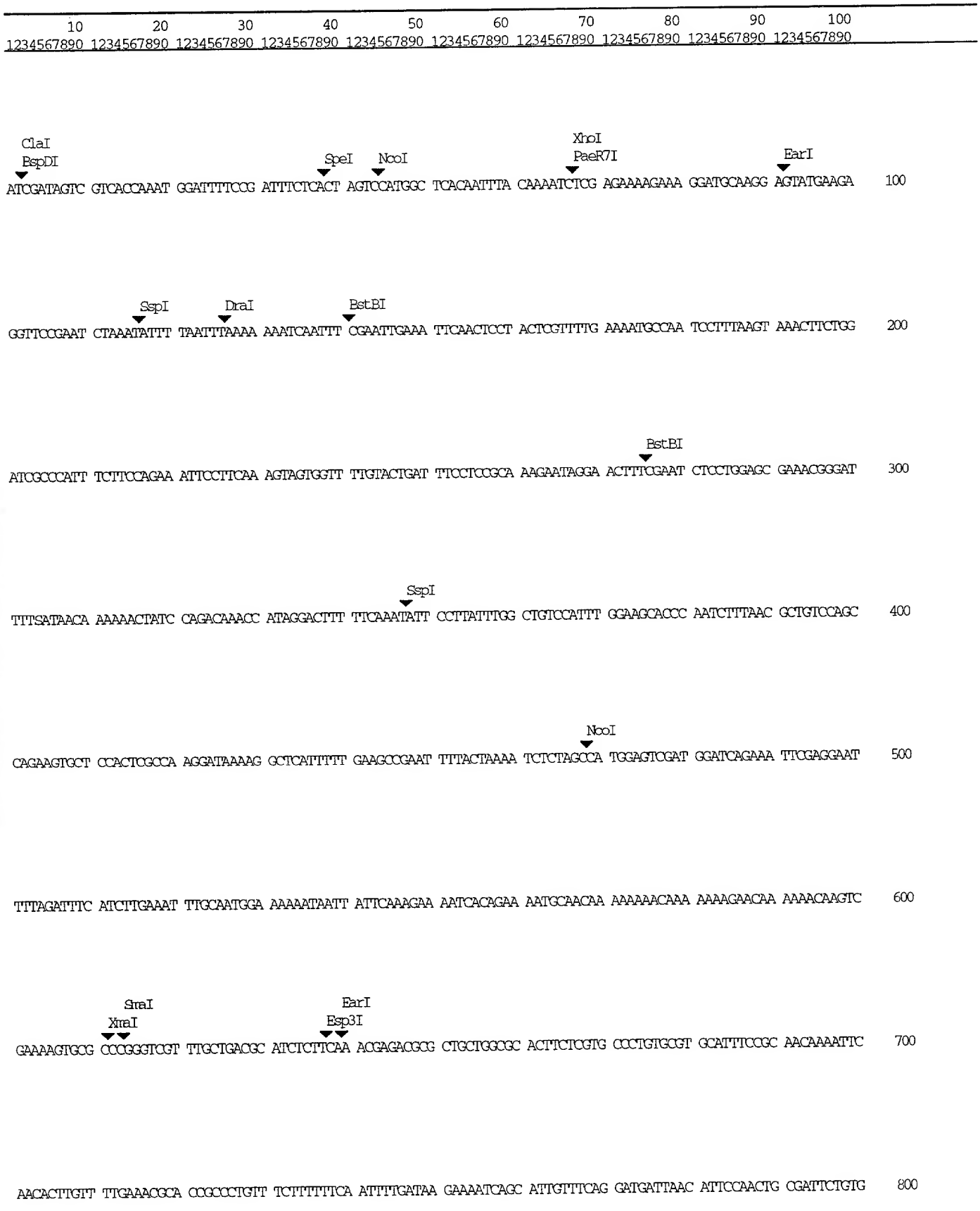
OFF
cell death

Fig. 1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SspI
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SmaI
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EarI
Esp3I
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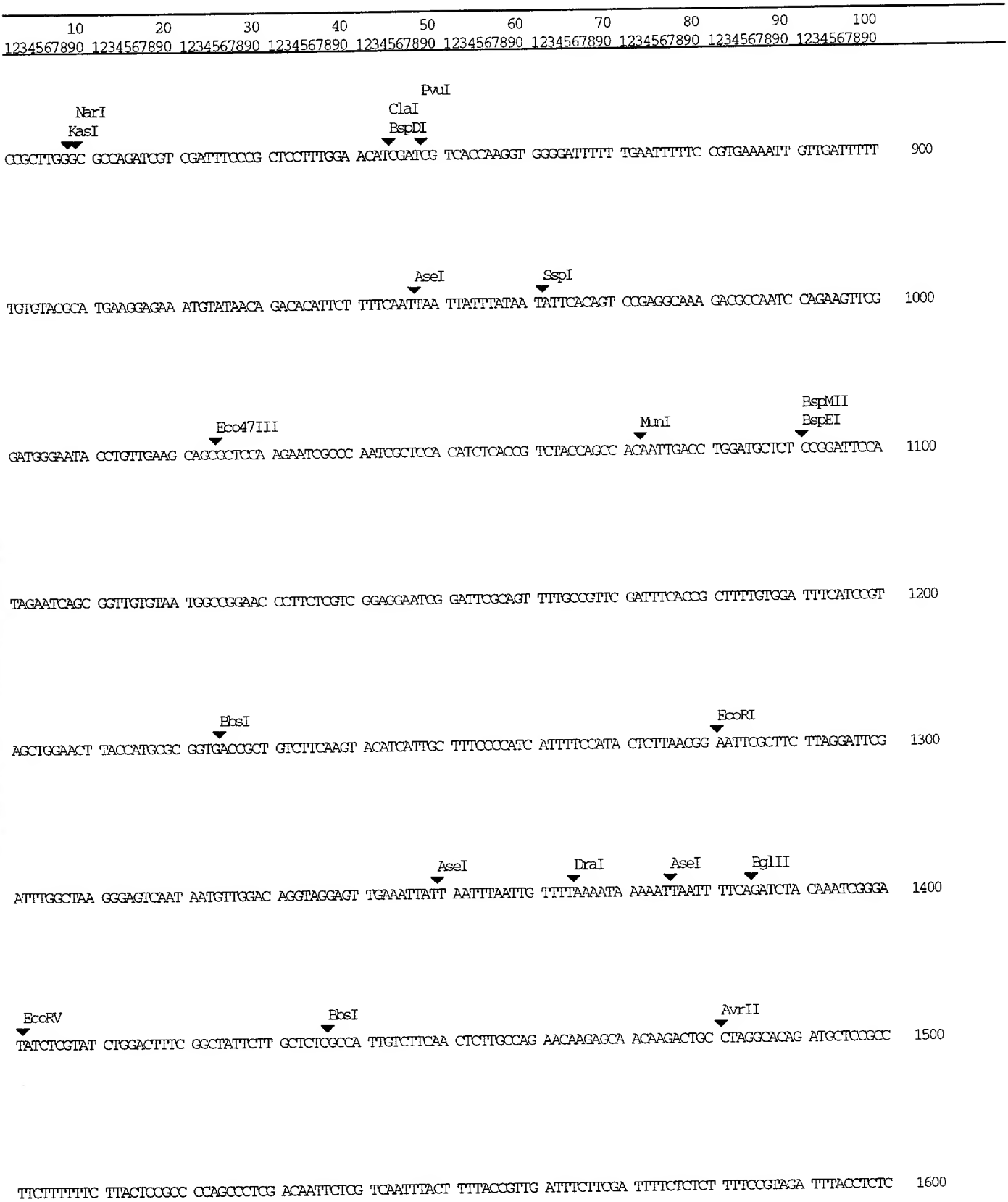
Fig. 2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AseI
SspI
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Eco47III
MunI
BspMII
BspEI
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DraI
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Fig. 2

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TCCGGCGTAT CGGCGACGAA CGATGGCGAC TGGCGAGATG AAGGAGTTTC TGGGGATAAA AGGCACAGAG CCCACCGATT TTGGAATCAA TAGTGATGCT 1800

MunI EarI

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EcoRV SalI

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AATGGAATGG TTTGGAGCAC CGGGATTGCC GTGTGGAGTG CAACCGGAGC ACGAAATGAT GCGAGTTATG GGAACGATAT TCGAGAAGAA GCACGCGGAA 2100

BsaI PvuII

AATTTTGAGA CCTTCTGTGA GCAGCTGCTC GCAGTGCCCA GAATCTCATT TTCACTGTAT CAGGATGTGG TTCGGACGGT TGGAAATGCA CAGACAGATC 2200

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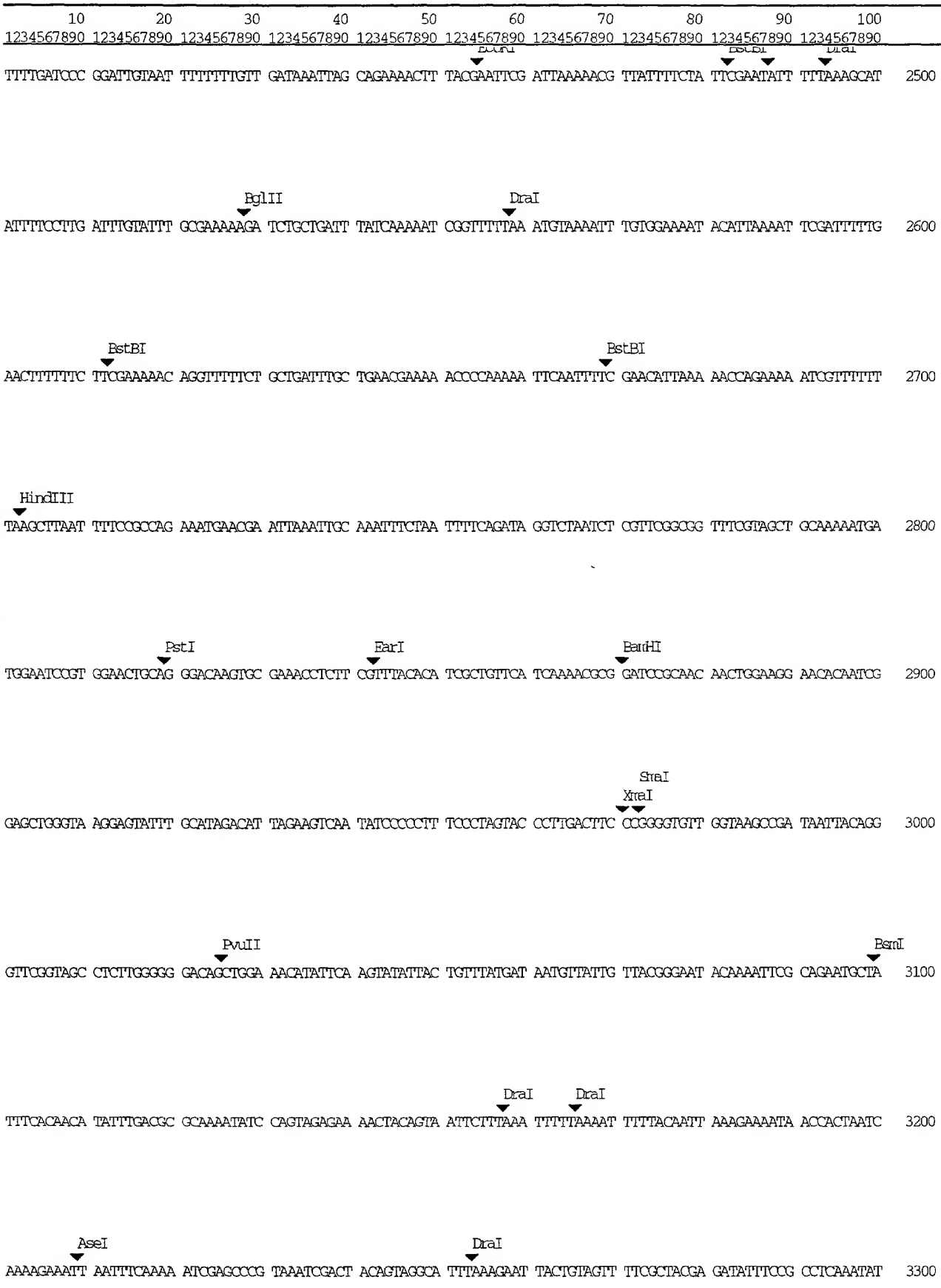
SspI

Fig. 2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DraI
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PstI
EarI
BamHI
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XmaI
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PvuII
BsmI
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DraI
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DraI
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Fig. 2

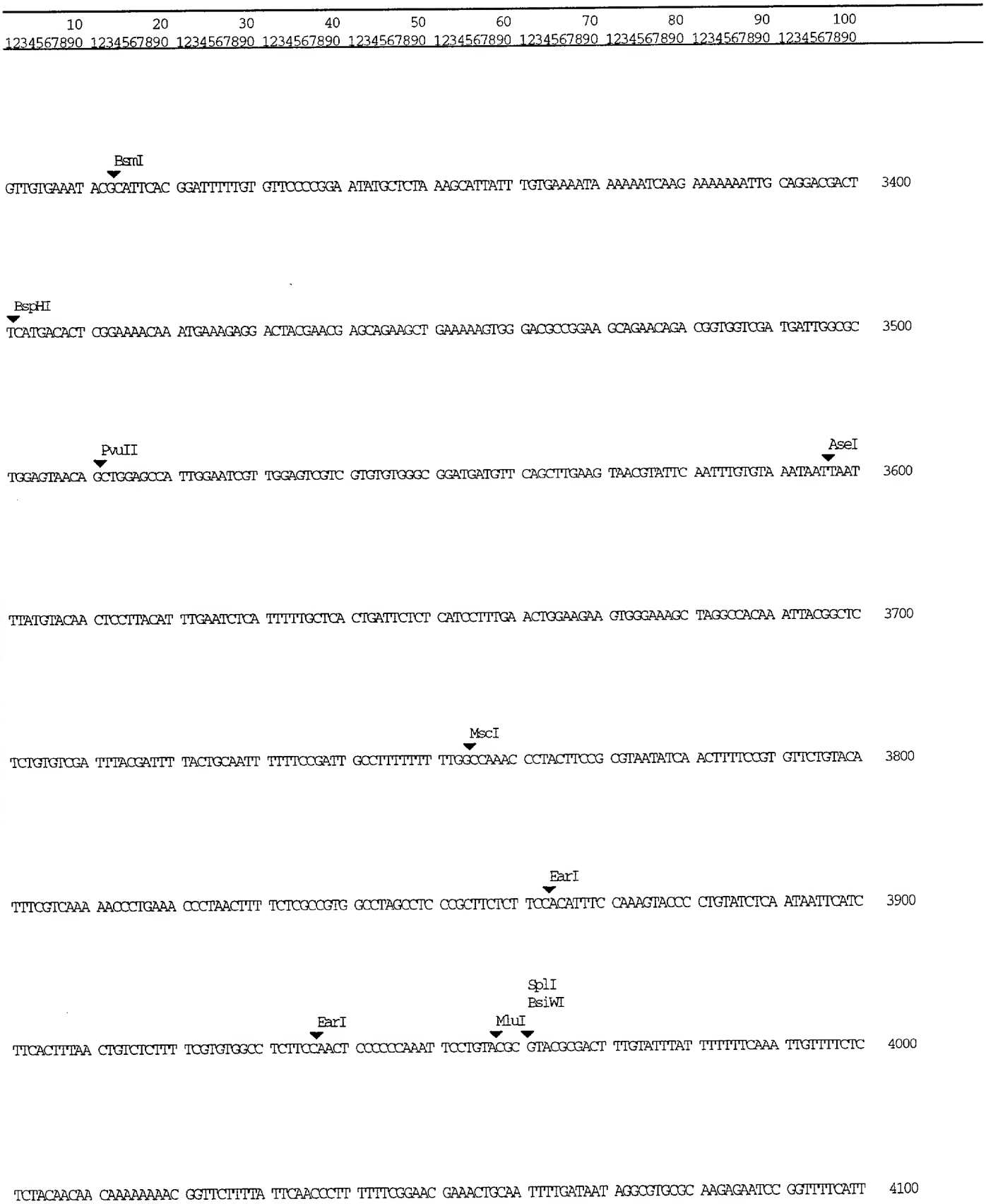
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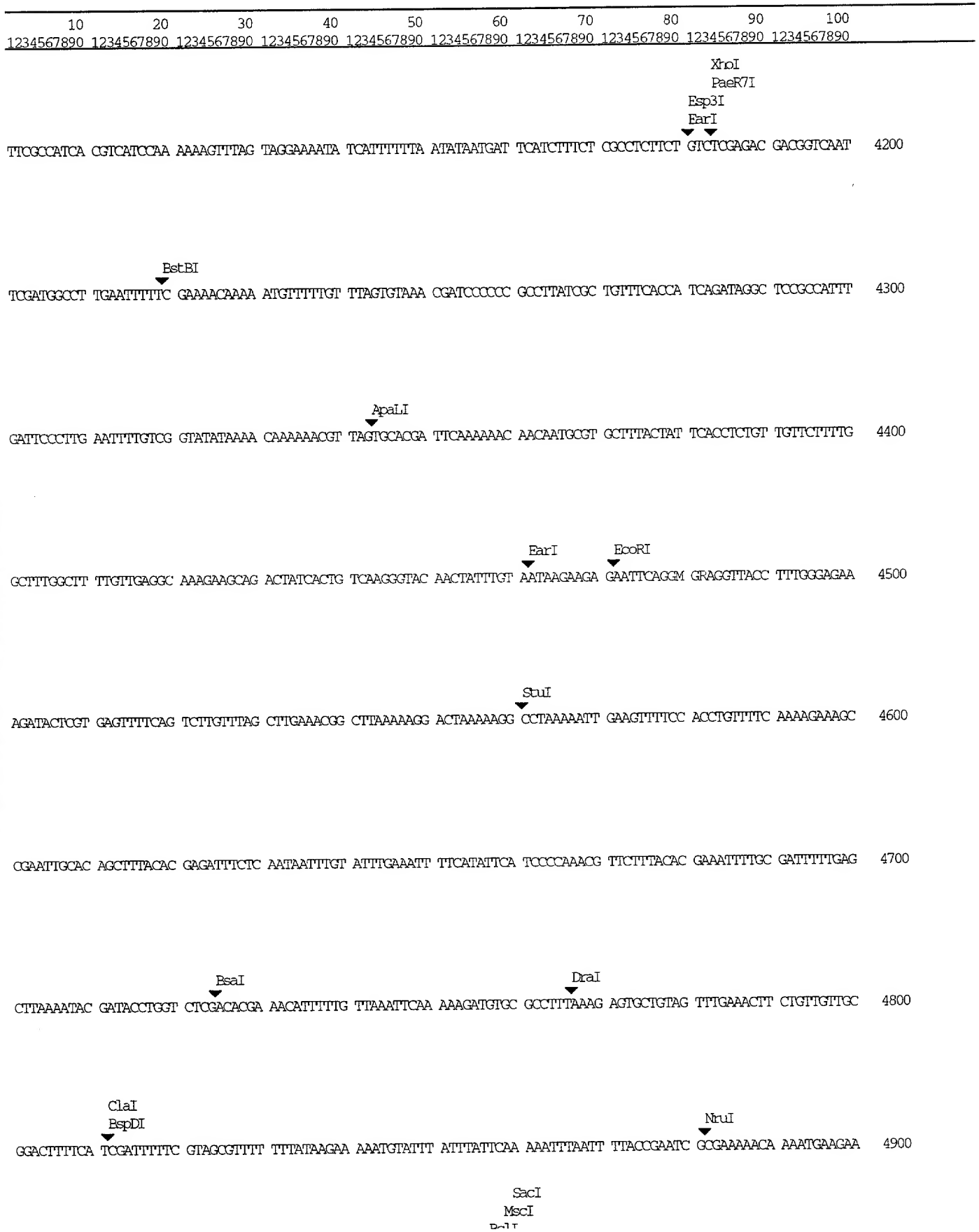
Fig. 2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SacI
MscI

Fig. 2

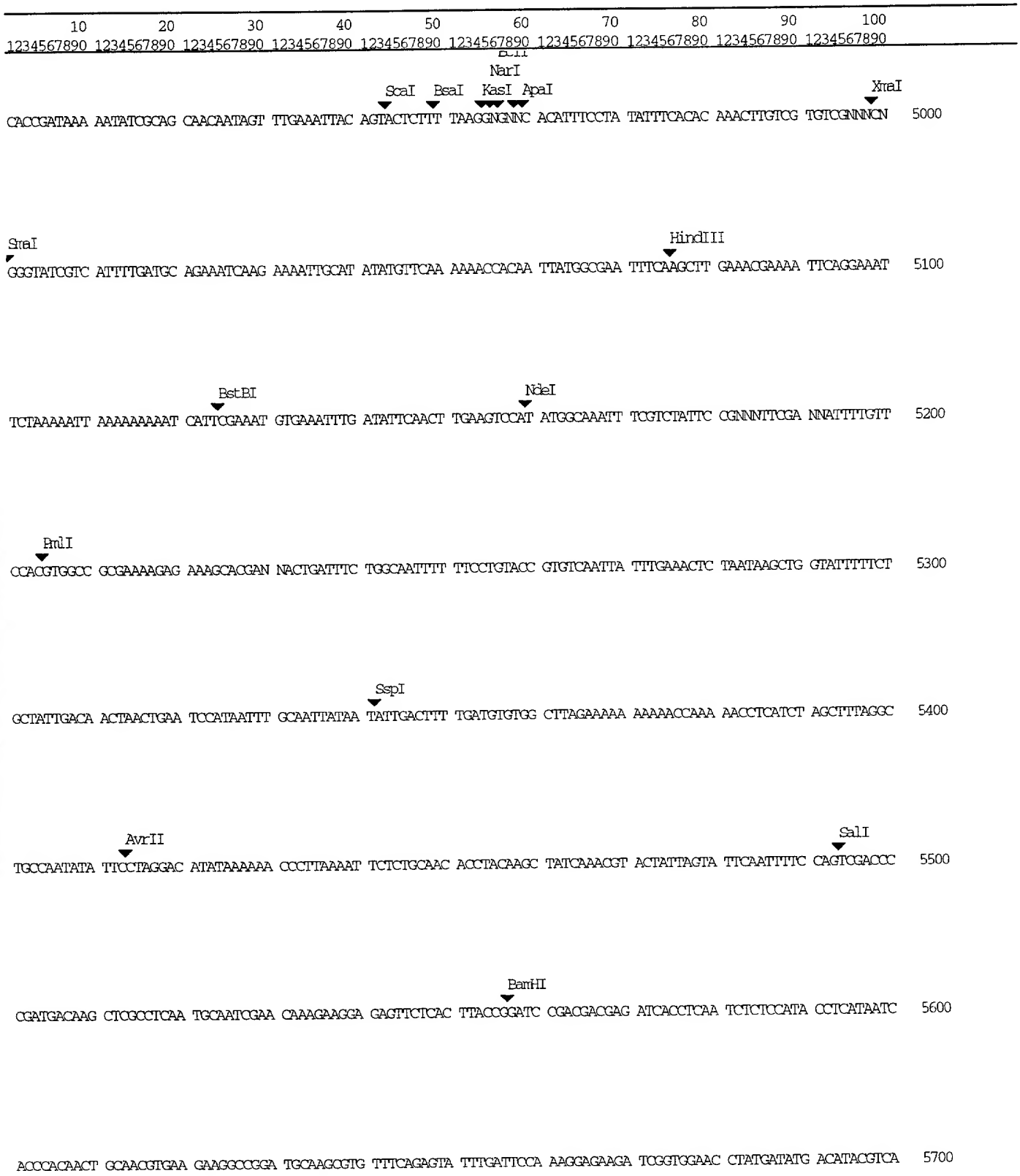
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Fig. 2

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AATTCAACAA TAAACTATTG GAAAACCGTT GAAATTTTAA CCTTGAACTG TAAGAAAAGT TGCGTGATTA TGTTGACAAT TTTGCCAAGT ATATCTTTGT   5900

 EcoRV                                SspI                  AseI             BsmI
GGATATCACA ATAAACGAAG TCAAAGCACG AAATATTACG GAAACACAAA ATTAATGAGA ATGCGCAACA TATTTGACCG CAAAATATCT CGTAGCGAAA   6000

                           Eco47III                SacI                                               SspI
CTACAGTAAT TCTTCAAAAG ACTACTGTAG CGCTGTGTCG ATTTACGAGC TCGATTTTTG AAATGAATCA GACTAGAAGA AAAGGAGGAA AATATTGAAC   6100

 MunI                                BbsI
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PstI                                                         DraI
GCGACCACTA TGACTGTGAT CGTGGCAAGA CCCACTCAGA AAACTACGTG TTCCTTTAAA CAAATACATT TTTAAGTATT GTAGGTATAA AAATTGTTGG   6400

NheI                     SalI                  BbsI                                             HindIII
CTAGCAGTCT AGGCTGCCTT TTTCAGTCGA CAAACTTCTA ATTTAATCGG CGGGTCTTCA AAAAGTCGTT TCTTTGAAAA TATAAAGCTT TATATATTTA   6500

                          EcoRV       SpeI
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Fig. 2

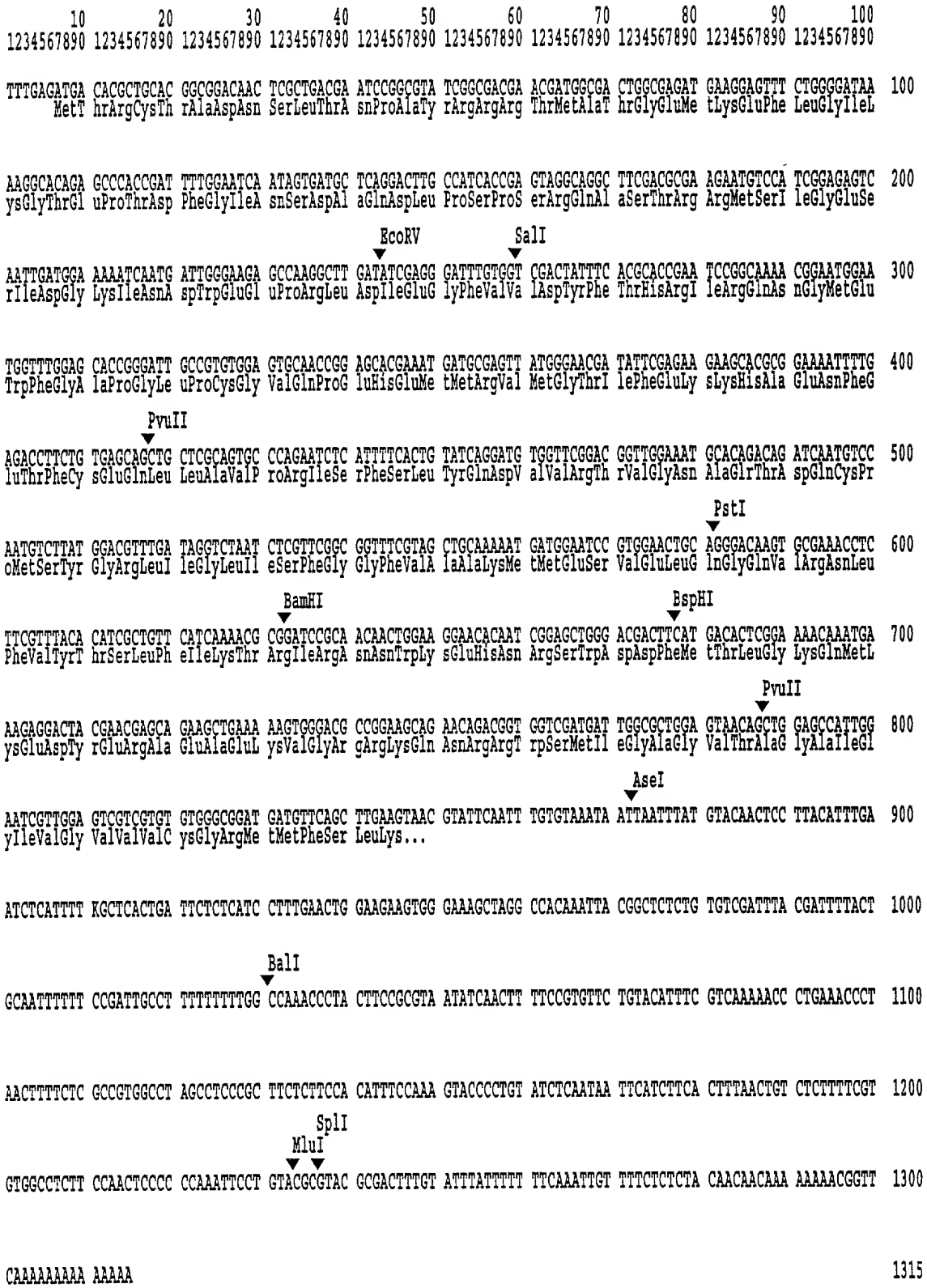

Fig. 3

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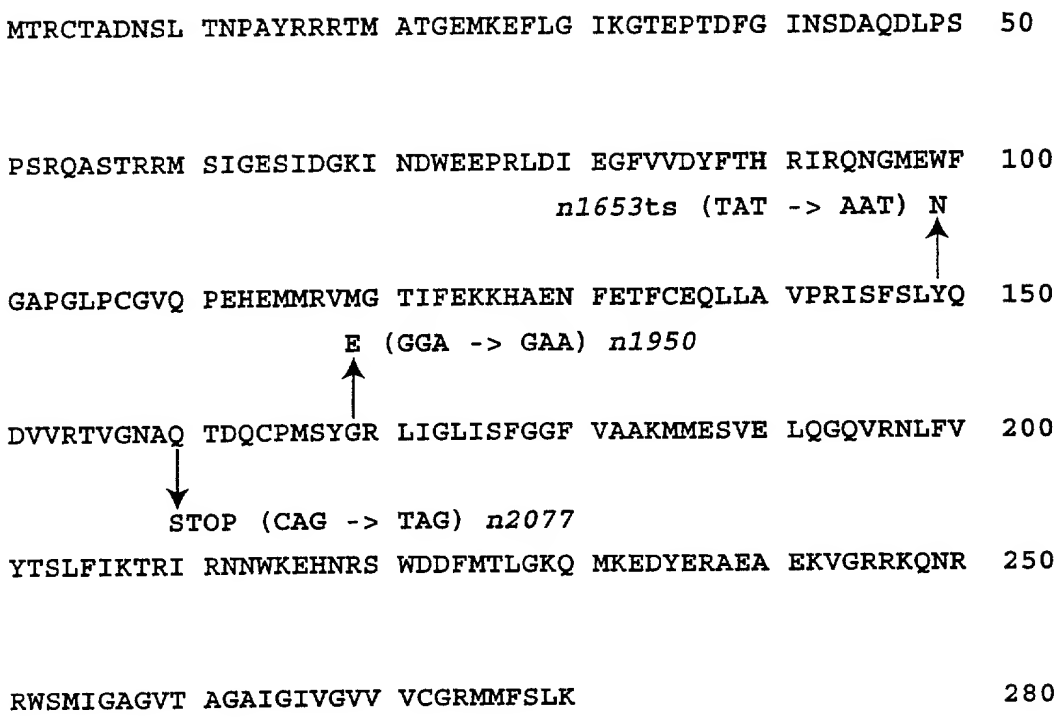
PSRQASTRRM	SIGESIDGKI	NDWEEPRLDI	EGFVVDYFTH	RIRQNGMEWF	100
GAPGLPCGVQ	PEHEMMRVMG	TTFEKKHAEN	FETFCEQLLA	VPRISFSLYQ	150
DVVRTVGNAQ	TDQCPMSYGR	LIGLISFGGF	VAAKMMESVE	LQGQVRNLFV	200
YTSLFIKTRI	RNNWKEHNRS	WDDFMTLGKQ	MKEDYERAEA	EKVGRRKQNR	250
RWSMIGAGVT	AGAIGIVGVV	VCGRMMFSLK			280

Fig. 4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GAPGLPCGVQ PEHEMMRVMG TIFEKKHAEN FETFCEQLLA VPRISFSLYQ 150
E (GGA -> GAA) n1950
DVVRTVGNAQ TDQCPMSYGR LIGLISFGGF VAAKMMESVE LQGQVRNLFV 200
STOP (CAG -> TAG) n2077
YTSLFIKTRI RNNWKEHNRS WDDFMTLGKQ MKEDYERAEA EKVGRRKQNR 250
RWSMIGAGVT AGAIGIVGVV VCGRMMFSLK 280

Fig. 5

Gap Weight:	3.000	Average Match:	0.540
Length Weight:	0.100	Average Mismatch:	-0.396
Quality:	89.8	Length:	298
Ratio:	0.376	Gaps:	11
Percent Similarity:	47.059	Percent Identity:	23.077

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 1 MAHAGRTGYDNREIVMKYIHYKLSQRGYEW...DAGDVGAAPPGAAPAPG 47

38 DFGINSDAQDLPSPSRQASTRRMSIGESIDGKINDWEEPRLDIEGFVVDY 87
48 IFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAA.............. 81

88 FTHRIRQNGMEWFGAPGLPCGVQPEHEMMRVMGTIFEKKHAKNFETFCEQ 137
82 ............AGPALSPVPPVVHLALRQAGDDFSRRYRGDFAEMSSQ 118

138 LLAVPRISFSLYQDVVRTVGNAQTDQCPMSYGRLIGLISFGGFVAAKMME 187
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conserved residue mutated in *n1950*

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161 SVNREMSPLVDNIALWMTEYLNRHL.HTWIQDNGGWDAFVELYGPSMRPL 209

234 .DYERAEAEKVGRRKQNRRWSMIGAGVTAGAIGIVGVVVCGRMMFSLK 280
210 FDFSWLSLKTL......LSLALVGACITLGAY.....LSHK 239
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Fig. 6

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 51 GCCGCTCTCC GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA
101 GGTGCCGGGG CTCCGGGCCC TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC
151 GAACTGCGCG ACGGGAGGTC CGGGAGGCGA CCGTAGTCGC GCCGCCGCGC
201 AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG GGGTGCGCCG
251 GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC
301 ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC
351 TTCTCCCCAC CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG
401 GCACCGGCGG GCCAGGCGCG TCCTGCCTTC ATTTATCCAG CAGCTTTTCG
451 GAAAATGCAT TTGCTGTTCG GAGTTTAATC AGAAGACGAT TCCTGCCTCC
```

Fig. 7-1

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551 CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT

601 GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA

651 ATACCGGACT GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA

701 AACTCGAGCT CTTGAGATCT CCGGTTGGGA TTCCTGCGGA TTGACATTTC

751 TGTGAAGCAG AAGTCTGGGA ATCGATCTGG AAATCCTCCT AATTTTTACT

801 CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA TCAGCTATAA

851 CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG

901 GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA

951 CAAGTAAGTC TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC

1001 CTTTGAGATT TTTTACTTAA AGTGCATTCG AGTAAATTTA ATTTCCAGGC

1051 AGCTTAATAC ATTGTTTTTA GCCGTGTTAC TTGTAGTGTG TATGCCCTGC

1101 TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA CTTATTAGTT

1151 TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA

1201 CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA

1251 TTGGAATAAA AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC

1301 AAGTGTTCCG CGTGATTGAA GACACCCCCT CGTCCAAGAA TGCAAAGCAC

1351 ATCCAATAAA ATAGCTGGAT TATAACTCCT CTTCTTTCTC TGGGGGCCGT

1401 GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT GCTTTTCCTC

1451 TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA

1501 GTGATGAAGT ACATCCATTA TAAGCTGTCG CAGAGGGGCT ACGAGTGGGA

1551 TGCGGGAGAT GTGGGCGCCG CGCCCCCGGG GGCCGCCCCC GCACCGGGCA

1601 TCTTCTCCTC CCAGCCCGGG CACACGCCCC ATCCAGCCGC ATCCCGCGAC

1651 CCGGTCGCCA GGACCTCGCC GCTGCAGACC CCGGCTGCCC CCGGCGCCGC

1701 CGCGGGGCCT GCGCTCAGCC CGGTGCCACC TGTGGTCCAC CTGGCCCTCC

1751 GCCAAGCCGG CGACGACTTC TCCCGCCGCT ACCGCGGCGA CTTCGCCGAG

1801 ATGTCCAGCC AGCTGCACCT GACGCCCTTC ACCGCGCGGG GACGCTTTGC

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1901 TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG CGTCAACCGG

Fig. 7-2

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2001 GAACCGGCAC CTGCACACCT GGATCCAGGA TAACGGAGGC TGGGATGCCT
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2101 CTGTCTCTGA AGACTCTGCT CAGTTTGGCC CTGGTGGGAG CTTGCATCAC
2151 CCTGGGTGCC TATCTGAGCC ACAAGTGAAG TCAACATGCC TGCCCCAAAC
2201 AAATATGCAA AAGGTTCACT AAAGCAGTAG AAATAATATG CATTGTCAGT
2251 GATGTACCAT GAAACAAAGC TGCAGGCTGT TTAAGAAAAA ATAACACACA
2301 TATAAACATC ACACACACAG ACAGACACAC ACACACACAA CAATTAACAG
2351 TCTTCAGGCA AAACGTCGAA TCAGCTATTT ACTGCCAAAG GGAAATATCA
2401 TTTATTTTTT ACATTATTAA GAAAAAAGAT TTATTTATTT AAGACAGTCC
2451 CATCAAAACT CCGTCTTTGG AAATCCGACC ACTAATTGCC AAACACCGCT
2501 TCGTGTGGCT CCACCTGGAT GTTCTGTGCC TGTAAACATA GATTCGCTTT
2551 CCATGTTGTT GGCCGGATCA CCATCTGAAG AGCAGACGGA TGGAAAAAGG
2601 ACCTGATCAT TGGGGAAGCT GGCTTTCTGG CTGCTGGAGG CTGGGGAGAA
2651 GGTGTTCATT CACTTGCATT TCTTTGCCCT GGGGGCGTGA TATTAACAGA
2701 GGGAGGGTTC CCGTGGGGGG AAGTCCATGC CTCCCTGGCC TGAAGAAGAG
2751 ACTCTTTGCA TATGACTCAC ATGATGCATA CCTGGTGGGA GGAAAAGAGT
2801 TGGGAACTTC AGATGGACCT AGTACCCACT GAGATTTCCA CGCCGAAGGA
2851 CAGCGATGGG AAAAATGCCC TTAAATCATA GGAAAGTATT TTTTTAAGCT
2901 ACCAATTGTG CCGAGAAAAG CATTTTAGCA ATTTATACAA TATCATCCAG
2951 TACCTTAAAC CCTGATTGTG TATATTCATA TATTTTGGAT ACGCACCCCC
3001 CAACTCCCAA TACTGGCTCT GTCTGAGTAA GAAACAGAAT CCTCTGGAAC
3051 TTGAGGAAGT GAACATTTCG GTGACTTCCG ATCAGGAAGG CTAGAGTTAC
3101 CCAGAGCATC AGGCCGCCAC AAGTGCCTGC TTTTAGGAGA CCGAAGTCCG
3151 CAGAACCTAC CTGTGTCCCA GCTTGGAGGC CTGGTCCTGG AACTGAGCCG
3201 GGCCCTCACT GGCCTCCTCC AGGGATGATC AACAGGGTAG TGTGGTCTCC
3251 GAATGTCTGG AAGCTGATGG ATGGAGCTCA GAATTCCACT GTCAAGAAAG
3301 AGCAGTAGAG GGGTGTGGCT GGGCCTGTCA CCCTGGGGCC CTCCAGGTAG
3351 GCCCGTTTTC ACGTGGAGCA TAGGAGCCAC GACCCTTCTT AAGACATGTA

Fig. 7-3

3401 TCACTGTAGA GGGAAGGAAC AGAGGCCCTG GGCCTTCCTA TCAGAAGGAC
3451 ATGGTGAAGG CTGGGAACGT GAGGAGAGGC AATGGCCACG GCCCATTTTG
3501 GCTGTAGCAC ATGGCACGTT GGCTGTGTGG CCTTGGCCAC CTGTGAGTTT
3551 AAAGCAAGGC TTTAAATGAC TTTGGAGAGG GTCACAAATC CTAAAAGAAG
3601 CATTGAAGTG AGGTGTCATG GATTAATTGA CCCCTGTCTA TGGAATTACA
3651 TGTAAAACAT TATCTTGTCA CTGTAGTTTG GTTTTATTTG AAAACCTGAC
3701 AAAAAAAAAG TTCCAGGTGT GGAATATGGG GGTTATCTGT ACATCCTGGG
3751 GCATTAAAAA AAAATCAATG GTGGGGAACT ATAAAGAAGT AACAAAAGAA
3801 GTGACATCTT CAGCAAATAA ACTAGGAAAT TTTTTTTTCT TCCAGTTTAG
3851 AATCAGCCTT GAAACATTGA TGGAATAACT CTGTGGCATT ATTGCATTAT
3901 ATACCATTTA TCTGTATTAA CTTTGGAATG TACTCTGTTC AATGTTTAAT
3951 GCTGTGGTTG ATATTTCGAA AGCTGCTTTA AAAAAATACA TGCATCTCAG
4001 CGTTTTTTTG TTTTTAATTG TATTTAGTTA TGGCCTATAC ACTATTTGTG
4051 AGCAAAGGTG ATCGTTTTCT GTTTGAGATT TTTATCTCTT GATTCTTCAA
4101 AAGCATTCTG AGAAGGTGAG ATAAGCCCTG AGTCTCAGCT ACCTAAGAAA
4151 AACCTGGATG TCACTGGCCA CTGAGGAGCT TTGTTTCAAC CAAGTCATGT
4201 GCATTTCCAC GTCAACAGAA TTGTTTATTG TGACAGTTAT ATCTGTTGTC
4251 CCTTTGACCT TGTTTCTTGA AGGTTTCCTC GTCCCTGGGC AATTCCGCAT
4301 TTAATTCATG GTATTCAGGA TTACATGCAT GTTTGGTTAA ACCCATGAGA
4351 TTCATTCAGT TAAAAATCCA GATGGCGAAT GACCAGCAGA TTCAAATCTA
4401 TGGTGGTTTG ACCTTTAGAG AGTTGCTTTA CGTGGCCTGT TTCAACACAG
4451 ACCCACCCAG AGCCCTCCTG CCCTCCTTCC GCGGGGGCTT TCTCATGGCT
4501 GTCCTTCAGG GTCTTCCTGA AATGCAGTGG TCGTTACGCT CCACCAAGAA
4551 AGCAGGAAAC CTGTGGTATG AAGCCAGACC TCCCCGGCGG GCCTCAGGGA
4601 ACAGAATGAT CAGACCTTTG AATGATTCTA ATTTTTAAGC AAAATATTAT
4651 TTTATGAAAG GTTTACATTG TCAAAGTGAT GAATATGGAA TATCCAATCC
4701 TGTGCTGCTA TCCTGCCAAA ATCATTTTAA TGGAGTCAGT TTGCAGTATG
4751 CTCCACGTGG TAAGATCCTC CAAGCTGCTT TAGAAGTAAC AATGAAGAAC
4801 GTGGACGTTT TTAATATAAA GCCTGTTTTG TCTTTTGTTG TTGTTCAAAC

Fig. 7-4

4851 GGGATTCACA GAGTATTTGA AAAATGTATA TATATTAAGA GGTCACGGGG
4901 GCTAATTGCT AGCTGGCTGC CTTTTGCTGT GGGGTTTTGT TACCTGGTTT
4951 TAATAACAGT AAATGTGCCC AGCCTCTTGG CCCCAGAACT GTACAGTATT
5001 GTGGCTGCAC TTGCTCTAAG AGTAGTTGAT GTTGCATTTT CCTTATTGTT
5051 AAAAACATGT TAGAAGCAAT GAATGTATAT AAAAGC

Fig. 7-5

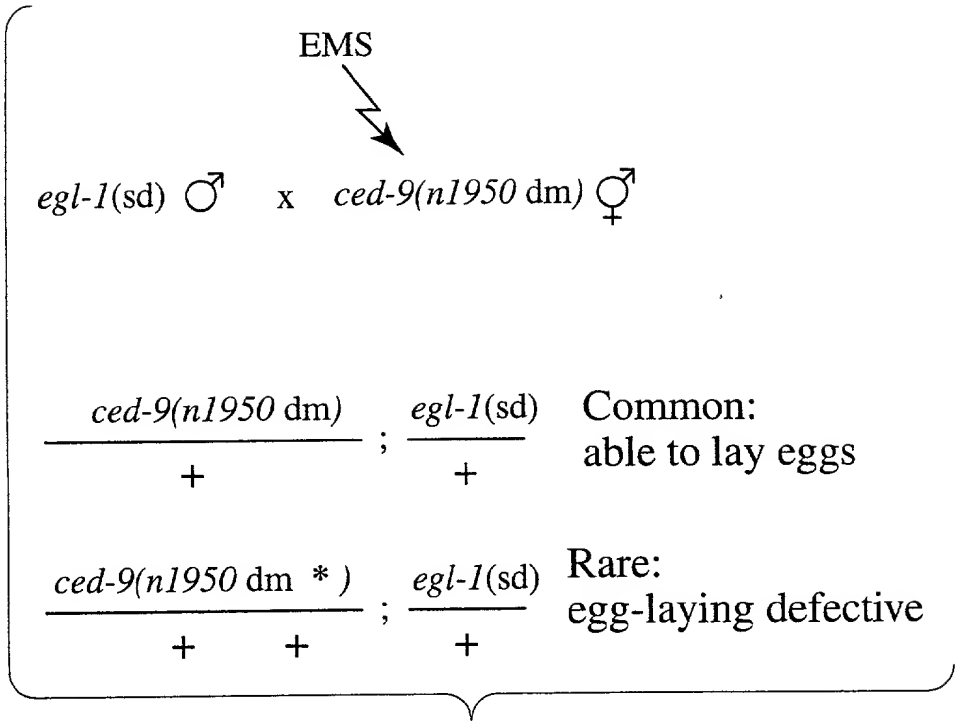

EMS
egl-1(sd) ♂ x ced-9(n1950 dm) ♀
ced-9(n1950 dm) / + ; egl-1(sd) / +
Common:
able to lay eggs
ced-9(n1950 dm *) / + + ; egl-1(sd) / +
Rare:
egg-laying defective

Fig. 8

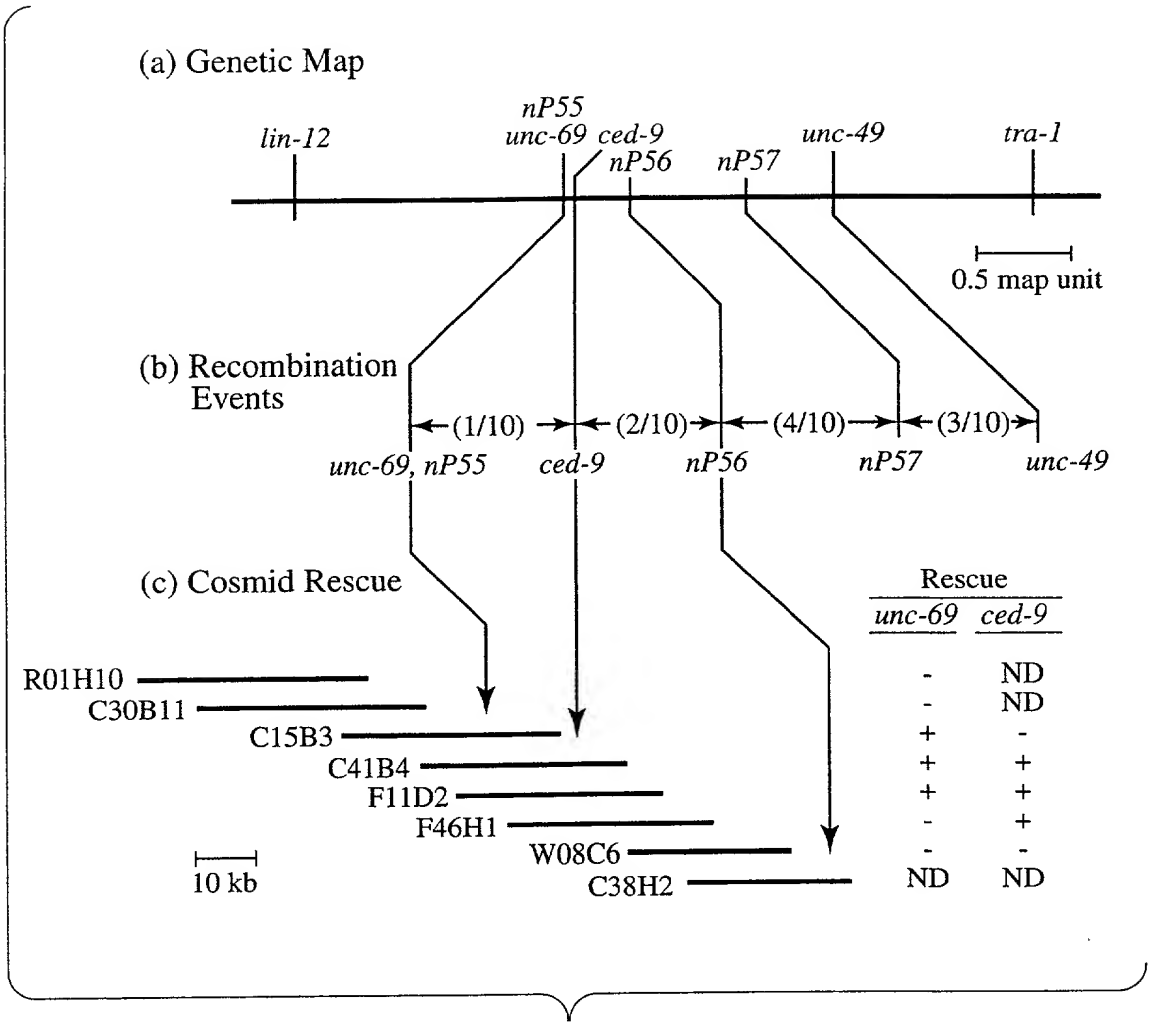

(a) Genetic Map
lin-12
nP55
unc-69
ced-9
nP56
nP57
unc-49
tra-1
0.5 map unit
(b) Recombination Events
(1/10)
(2/10)
(4/10)
(3/10)
unc-69, nP55
ced-9
nP56
nP57
unc-49
(c) Cosmid Rescue
Rescue
unc-69
ced-9
R01H10 - ND
C30B11 - ND
C15B3 + -
C41B4 + +
F11D2 + +
F46H1 - +
W08C6 - -
C38H2 ND ND
10 kb

Fig. 9

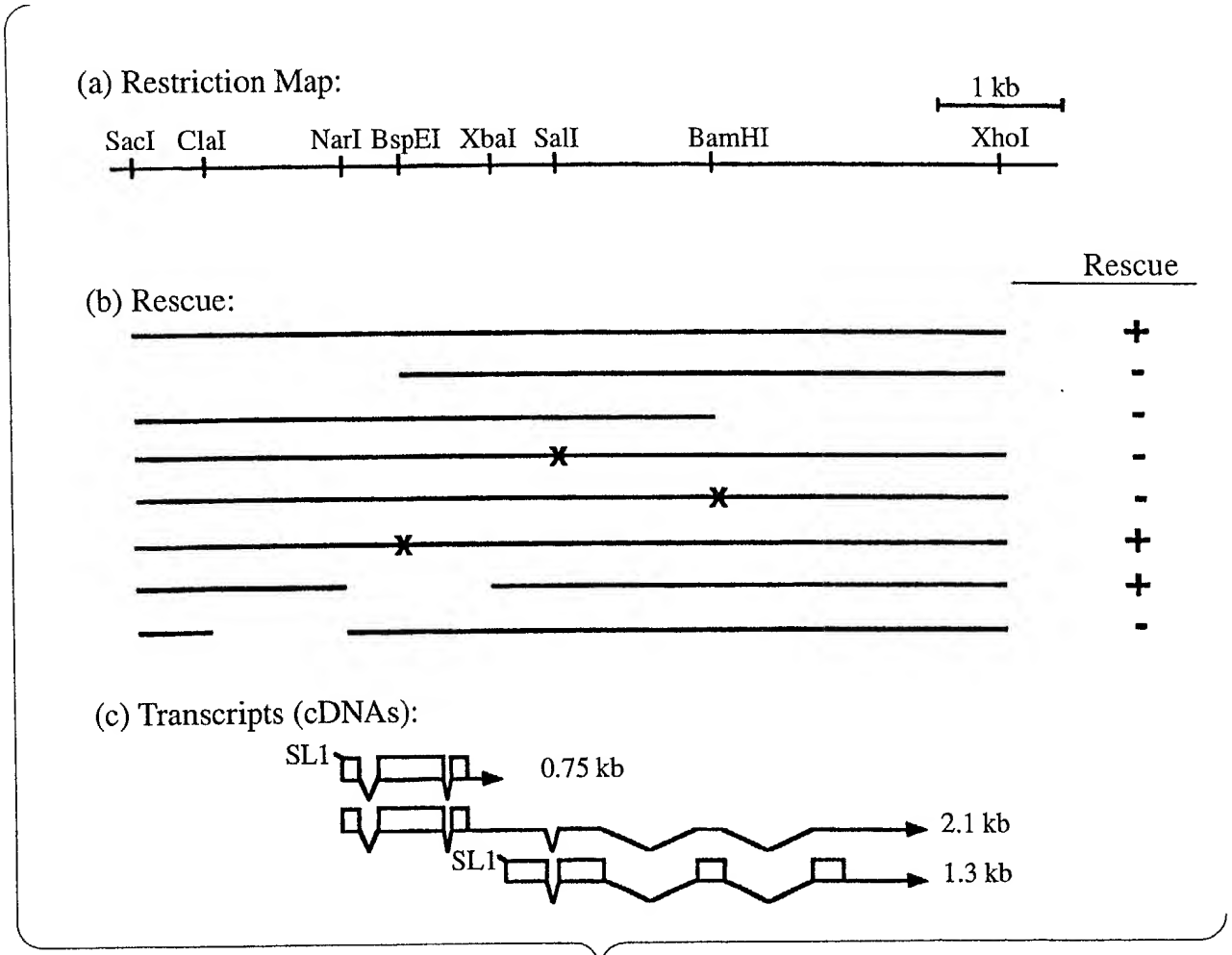
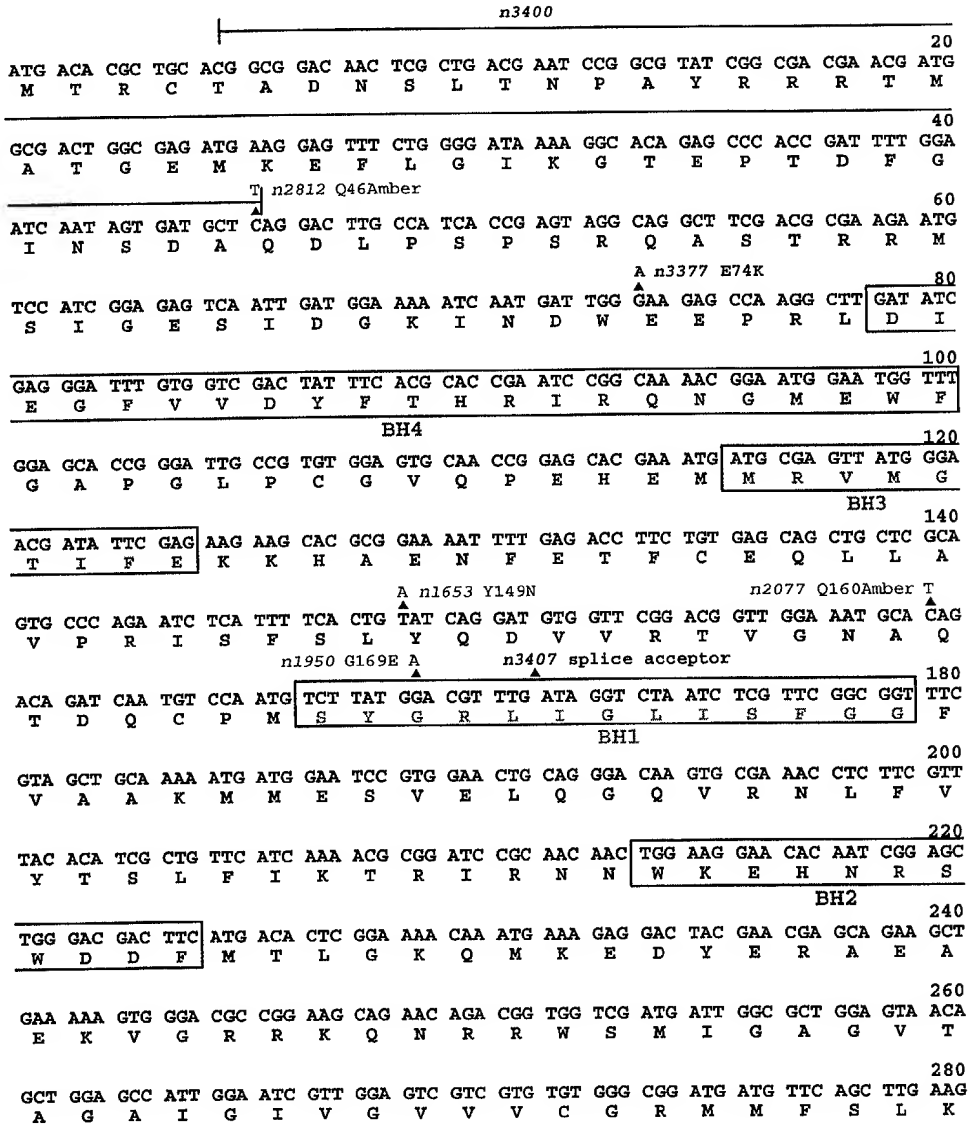


Fig. 10

Figure 11


n3400
n2812 Q46Amber
A n3377 E74K
BH4
BH3
A n1653 Y149N
n2077 Q160Amber T
n1950 G169E A
n3407 splice acceptor
BH1
BH2